M. Monshipouri

ENTERED

1600

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 1 <110> APPLICANT: Cobb, Melanie
 2 <120> TITLE OF INVENTION: TAO PROTEIN KINASE POLYPEPTIDES AND METHODS OF USE THEREOF
 3 <130> FILE REFERENCE: 10624-026-999
 4 <140> CURRENT APPLICATION NUMBER: US/09/686,346A
 5 <141> CURRENT FILING DATE: 2000-10-10
 6 <150> PRIOR APPLICATION NUMBER: 09/060,410
 7 <151> PRIOR FILING DATE: 1998-04-14
 8 <160> NUMBER OF SEQ ID NOS: 26
 9 <170> SOFTWARE: PatentIn version 3.0
11 <210> SEQ ID NO: 1
12 <211> LENGTH: 3312
13 <212> TYPE: DNA
14 <213> ORGANISM: Rattus norvegicus
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18      atgccatcaa ctaacagagc aggcagtcta aaggaccctg aaatcgcaga gctcttcttc     180
19      aaagaagatc cggaaaaact cttcacagat ctcagagaaa tcggccatgg gagctttgga     240
20      gcagtttatt ttgcacgaga tgtgcgtact aatgaagtgg tggccatcaa gaaaatgtct     300
21      tatagtggaa agcagtctac tgagaaatgg caggatatta ttaaggaagt caagtttcta     360
22      caaagaataa aacatcccaa cagtatagaa tacaaaggct gctatttacg tgaacacaca     420
23      gcatggcttg taatggaata ttgtttagga tctgcttcgg atttactaga agttcataaa     480
24      aagccattac aagaagtgga aatagcagca attacacatg gtgctctcca gggattagct     540
25      tatttacatt ctcataccat gatccataga gatatcaaag caggaaatat ccttctgaca     600
26      gaaccaggcc aagtgaaact tgctgacttt ggatctgctt ccatggcctc ccctgccaat     660
27      tcttttgtgg gaacaccata ttggatggcc ccagaagtaa tttttagccat ggatgaagga     720
28      caatatgatg gcaaagttga tgtatggtct cttggaataa catgtattga attagccgag     780
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31      tgcctccaga aaatccctca agatcgccct acatcagagg aactttttaaa gcacatgttt     960
32      gttcttcgag agcgccctga aacagtgtta atagatctta ttcaaaggac aaaggatgca    1020
33      gtaagagagc tggacaatct acaatatcga aagatgaaga aactccttttt ccaggaggca    1080
34      cataatggac cagcagtaga agcacaggaa gaagaggagg agcaagatca tggtggtggc    1140
35      cggacaggaa cagtaaatag tgttggaagc aatcagtcta tccccagtat gtctatcagt    1200
36      gccagtagcc aaagcagcag tgttaatagt cttccagatg catcggatga caagagtgag    1260
37      ctagacatga tggagggaga ccatacagtg atgtctaaca gttctgtcat ccacttaaaa    1320
38      cctgaggagg aaaattacca agaagaagga gatcctagaa caagagcatc agctccacag    1380
39      tctccacctc aagtgtctcg tcacaaatca cattatcgta atagagaaca ctttgcaact    1440
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41      agagaacaga tgtctggtta taagcggatg aggcgacagc atcagaagca gctgatgact    1560
42      ctggaaaata aactgaaggc agaaatggac gaacatcggc tcagattaga caaagatctt    1620
43      gaaactcagc gcaacaattt cgctgcagaa atggagaaac ttattaagaa acaccaagct    1680
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RAW SEQUENCE LISTING   DATE: 09/10/2003
PATENT APPLICATION: **US/09/686,346A**   TIME: 09:44:48

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Output Set: **N:\CRF4\09102003\I686346A.raw**

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48	gctaatcttc	ttcgacgtca	aaggcagtat	ctagagctag	aatgtcgtcg	cttcaaaaga	1980
49	agaatgttac	ttggtcggca	taacttggaa	caggaccttg	tcagggagga	gttaaacaaa	2040
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52	caacatcaaa	ctgagcttac	taaccagctg	gaatacaata	agagaaggga	acgggaacta	2220
53	agacggaaac	atgtcatgga	agttcgacag	cagcctaaga	gtttgaagtc	taaagaactc	2280
54	caaataaaaa	agcagtttca	ggatacctgc	aaaattcaaa	ccagacagta	caaagcatta	2340
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57	gaaatgctct	ccacacaagc	tctgcgtttg	gatgaagcac	aggaagcaga	atgccaggtt	2520
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60	cggagagcac	tcttagaaca	gaagattgaa	gaagagatgt	tggctttgca	gaatgaacgc	2700
61	acagaacgaa	tacgtagcct	gctcgagcgc	caggccagag	aaattgaagc	tttttgactct	2760
62	gaaagcatga	gattaggttt	tagtaacatg	gtcctttcta	atctctcccc	tgaggcattc	2820
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65	ccccaaccat	ggggtcaccc	ctcagggcca	atgcaagggg	tacctcgagg	tagcagtata	3000
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69	acatcagcac	agcagcctcc	tcacttgggt	actaccgggt	ggaagctgtg	catatggtat	3240
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73 <210> SEQ ID NO: 2
74 <211> LENGTH: 1001
75 <212> TYPE: PRT
76 <213> ORGANISM: Rattus norvegicus
77 <400> SEQUENCE: 2 .

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81                     20                  25                  30
82     Glu Ile Gly His Gly Ser Phe Gly Ala Val Tyr Phe Ala Arg Asp Val
83                 35                  40                  45
84     Arg Thr Asn Glu Val Val Ala Ile Lys Lys Met Ser Tyr Ser Gly Lys
85             50                  55                  60
86     Gln Ser Thr Glu Lys Trp Gln Asp Ile Ile Lys Glu Val Lys Phe Leu
87     65                  70                  75                  80
88     Gln Arg Ile Lys His Pro Asn Ser Ile Glu Tyr Lys Gly Cys Tyr Leu
89                     85                  90                  95
90     Arg Glu His Thr Ala Trp Leu Val Met Glu Tyr Cys Leu Gly Ser Ala
91                 100                 105                 110
92     Ser Asp Leu Leu Glu Val His Lys Lys Pro Leu Gln Glu Val Glu Ile
93             115                 120                 125
94     Ala Ala Ile Thr His Gly Ala Leu Gln Gly Leu Ala Tyr Leu His Ser
```

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95          130                135                140
96       His Thr Met Ile His Arg Asp Ile Lys Ala Gly Asn Ile Leu Leu Thr
97       145                150                155                160
98       Glu Pro Gly Gln Val Lys Leu Ala Asp Phe Gly Ser Ala Ser Met Ala
99                   165                170                175
100       Ser Pro Ala Asn Ser Phe Val Gly Thr Pro Tyr Trp Met Ala Pro Glu
101                   180                185                190
102       Val Ile Leu Ala Met Asp Glu Gly Gln Tyr Asp Gly Lys Val Asp Val
103                   195                200                205
104       Trp Ser Leu Gly Ile Thr Cys Ile Glu Leu Ala Glu Arg Lys Pro Pro
105             210                215                220
106       Leu Phe Asn Met Asn Ala Met Ser Ala Leu Tyr His Ile Ala Gln Asn
107       225                230                235                240
108       Glu Ser Pro Thr Leu Gln Ser Asn Glu Trp Ser Asp Tyr Phe Arg Asn
109                   245                250                255
110       Phe Val Asp Ser Cys Leu Gln Lys Ile Pro Gln Asp Arg Pro Thr Ser
111                   260                265                270
112       Glu Glu Leu Leu Lys His Met Phe Val Leu Arg Glu Arg Pro Glu Thr
113             275                280                285
114       Val Leu Ile Asp Leu Ile Gln Arg Thr Lys Asp Ala Val Arg Glu Leu
115             290                295                300
116       Asp Asn Leu Gln Tyr Arg Lys Met Lys Lys Leu Leu Phe Gln Glu Ala
117       305                310                315                320
118       His Asn Gly Pro Ala Val Glu Ala Gln Glu Glu Glu Glu Glu Gln Asp
119                   325                330                335
120       His Gly Gly Gly Arg Thr Gly Thr Val Asn Ser Val Gly Ser Asn Gln
121             340                345                350
122       Ser Ile Pro Ser Met Ser Ile Ser Ala Ser Ser Gln Ser Ser Ser Val
123             355                360                365
124       Asn Ser Leu Pro Asp Ala Ser Asp Asp Lys Ser Glu Leu Asp Met Met
125             370                375                380
126       Glu Gly Asp His Thr Val Met Ser Asn Ser Ser Val Ile His Leu Lys
127       385                390                395                400
128       Pro Glu Glu Glu Asn Tyr Gln Glu Glu Gly Asp Pro Arg Thr Arg Ala
129                   405                410                415
130       Ser Ala Pro Gln Ser Pro Pro Gln Val Ser Arg His Lys Ser His Tyr
131             420                425                430
132       Arg Asn Arg Glu His Phe Ala Thr Ile Arg Thr Ala Ser Leu Val Thr
133             435                440                445
134       Arg Gln Met Gln Glu His Glu Gln Asp Ser Glu Leu Arg Glu Gln Met
135             450                455                460
136       Ser Gly Tyr Lys Arg Met Arg Arg Gln His Gln Lys Gln Leu Met Thr
137       465                470                475                480
138       Leu Glu Asn Lys Leu Lys Ala Glu Met Asp Glu His Arg Leu Arg Leu
139                   485                490                495
140       Asp Lys Asp Leu Glu Thr Gln Arg Asn Asn Phe Ala Ala Glu Met Glu
141                   500                505                510
142       Lys Leu Ile Lys Lys His Gln Ala Ser Met Glu Lys Glu Ala Lys Val
143             515                520                525
```

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144          Met Ala Asn Glu Glu Lys Lys Phe Gln Gln His Ile Gln Ala Gln Gln
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146          Lys Lys Glu Leu Asn Ser Phe Leu Glu Ser Gln Lys Arg Glu Tyr Lys
147          545                 550                 555                 560
148          Leu Arg Lys Glu Gln Leu Lys Glu Glu Leu Asn Glu Asn Gln Ser Thr
149                          565                 570                 575
150          Pro Lys Lys Glu Lys Gln Glu Trp Leu Ser Lys Gln Lys Glu Asn Ile
151                          580                 585                 590
152          Gln His Phe Gln Ala Glu Glu Glu Ala Asn Leu Leu Arg Arg Gln Arg
153                          595                 600                 605
154          Gln Tyr Leu Glu Leu Glu Cys Arg Arg Phe Lys Arg Arg Met Leu Leu
155              610                 615                 620
156          Gly Arg His Asn Leu Glu Gln Asp Leu Val Arg Glu Glu Leu Asn Lys
157          625                 630                 635                 640
158          Arg Gln Thr Gln Lys Asp Leu Glu His Ala Met Leu Leu Arg Gln His
159                          645                 650                 655
160          Glu Ser Met Gln Glu Leu Glu Phe Arg His Leu Asn Thr Ile Gln Lys
161                          660                 665                 670
162          Met Arg Cys Glu Leu Ile Arg Leu Gln His Gln Thr Glu Leu Thr Asn
163                          675                 680                 685
164          Gln Leu Glu Tyr Asn Lys Arg Arg Glu Arg Glu Leu Arg Arg Lys His
165              690                 695                 700
166          Val Met Glu Val Arg Gln Gln Pro Lys Ser Leu Lys Ser Lys Glu Leu
167          705                 710                 715                 720
168          Gln Ile Lys Lys Gln Phe Gln Asp Thr Cys Lys Ile Gln Thr Arg Gln
169                          725                 730                 735
170          Tyr Lys Ala Leu Arg Asn His Leu Leu Glu Thr Thr Pro Lys Ser Glu
171                          740                 745                 750
172          His Lys Ala Val Leu Lys Arg Leu Lys Glu Glu Gln Thr Arg Lys Leu
173              755                 760                 765
174          Ala Ile Leu Ala Glu Gln Tyr Asp His Ser Ile Asn Glu Met Leu Ser
175              770                 775                 780
176          Thr Gln Ala Leu Arg Leu Asp Glu Ala Gln Glu Ala Glu Cys Gln Val
177          785                 790                 795                 800
178          Leu Lys Met Gln Leu Gln Gln Glu Leu Glu Leu Leu Asn Ala Tyr Gln
179                          805                 810                 815
180          Ser Lys Ile Lys Met Gln Ala Glu Ala Gln His Asp Arg Glu Leu Arg
181                          820                 825                 830
182          Glu Leu Glu Gln Arg Val Ser Leu Arg Arg Ala Leu Leu Glu Gln Lys
183                          835                 840                 845
184          Ile Glu Glu Glu Met Leu Ala Leu Gln Asn Glu Arg Thr Glu Arg Ile
185              850                 855                 860
186          Arg Ser Leu Leu Glu Arg Gln Ala Arg Glu Ile Glu Ala Phe Asp Ser
187          865                 870                 875                 880
188          Glu Ser Met Arg Leu Gly Phe Ser Asn Met Val Leu Ser Asn Leu Ser
189                          885                 890                 895
190          Pro Glu Ala Phe Ser His Ser Tyr Pro Gly Ala Ser Ser Trp Ser His
191                          900                 905                 910
192          Asn Pro Thr Gly Gly Ser Gly Pro His Trp Gly His Pro Met Gly Gly
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RAW SEQUENCE LISTING   DATE: 09/10/2003
PATENT APPLICATION: **US/09/686,346A**   TIME: 09:44:48

Input Set : **N:\EBONY'S\US09686346A.raw.txt**
Output Set: **N:\CRF4\09102003\I686346A.raw**

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197       945                    950                    955                    960
198       Gly Val Arg Asn Ser Pro Gln Ala Leu Arg Arg Thr Ala Leu Gly Gly
199                    965                    970                    975
200       Arg Thr Glu Gln Gly Met Ser Arg Ser Thr Ser Val Thr Ser Gln Ile
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207 <212> TYPE: DNA
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213       ccaggggcca tcatgccagc tggggggccgg gccgggagcc tgaaggaccc tgatgtagct      240
214       gagctcttct tcaaagatga ccctgagaag cttttctctg acctccggga aattggccat      300
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218       agggagcaca cagcttggct ggtgatggag tattgcctgg gttcagcttc tgatcttctc      540
219       gaagtgcaca agaagccgct gcaggaggta gagattgcag ctgtgaccca tggtgcgctt      600
220       cagggcctgg cctatctaca ttcacacaac atgatccata gagatgtgaa ggctgggaac      660
221       atcttgctgt cagaaccagg cttggtgaaa ctgggggact ttggctccgc atccatcatg      720
222       gcacctgcca actcatttgt gggcactcca tactggatgg ctccagaggt gatcctagcc      780
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237       gtcagccgtc agatccagga gcatgagcag gactcggccc tgcgggagca actaagtggc     1680
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 09/10/2003
PATENT APPLICATION: **US/09/686,346A**   TIME: 09:44:49

Input Set : **N:\EBONY'S\US09686346A.raw.txt**
Output Set: **N:\CRF4\09102003\I686346A.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 5,92,138
Seq#:7; N Pos. 208,210,223
Seq#:10; N Pos. 192
Seq#:11; N Pos. 18
Seq#:19; N Pos. 24,31
Seq#:20; N Pos. 3,6,13,16,19
Seq#:21; N Pos. 11,14,18
Seq#:22; N Pos. 19,22

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 2

VARIABLE LOCATION SUMMARY   DATE: 09/10/2003
PATENT APPLICATION: US/09/686,346A   TIME: 09:44:49

Input Set : **N:\EBONY'S\US09686346A.raw.txt**
Output Set: **N:\CRF4\09102003\I686346A.raw**

Use of n's or Xaa's(NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
in <220> to <223> section, please explain location of n or Xaa, and which
residue n or Xaa represents.

Seq#:5; N Pos. 5,92,138
Seq#:7; N Pos. 208,210,223
Seq#:10; N Pos. 192
Seq#:11; N Pos. 18
Seq#:19; N Pos. 24,31
Seq#:20; N Pos. 3,6,13,16,19
Seq#:21; N Pos. 11,14,18
Seq#:22; N Pos. 19,22

VERIFICATION SUMMARY   DATE: 09/10/2003
PATENT APPLICATION: **US/09/686,346A**   TIME: 09:44:49

Input Set : **N:\EBONY'S\US09686346A.raw.txt**
Output Set: **N:\CRF4\09102003\I686346A.raw**

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L:422 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:5
L:422 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
M:341 Repeated in SeqNo=5
L:453 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:7
L:453 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:180
L:487 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:10
L:487 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:180
L:497 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:11
L:497 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:629 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:631 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:19
L:632 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:19
L:632 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0
L:640 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:642 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20
L:643 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:20
L:643 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0
L:651 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:653 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:21
L:654 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:21
L:654 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0
L:662 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:664 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:22
L:665 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:22
L:665 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0
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STATISTICS SUMMARY   DATE: 09/10/2003
PATENT APPLICATION: **US/09/686,346A**   TIME: 09:44:49

Input Set : **N:\EBONY'S\US09686346A.raw.txt**
Output Set: **N:\CRF4\09102003\I686346A.raw**

Application Serial Number: US/09/686,346A
Alpha or Numeric or Xml: Numeric
Application Class:
Application File Date: 10-10-2000
Art Unit: 1600
Software Application: PatentIN3.0
Total Number of Sequences: 26
Total Nucleotides: 9901
Total Amino Acids: 2612
Number of Errors: 0
Number of Warnings: 26
Number of Corrections: 1

MESSAGE SUMMARY

258 W: 12 (Mandatory Feature missing)
270 C: 1 (Current Application Number differs)
281 W: 4 (Numeric Fields not Ordered)
341 W: 10 ((46) "n" or "Xaa" used)